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AN   2002114459   CANCERLIT
DN   21638384   PubMed ID: 11606564
TI   Phosphorylation of Ser307 in insulin receptor substrate-1 blocks
     interactions with the insulin receptor and inhibits insulin action.
AU   Aguirre Vincent; Werner Eric D; Giraud Jodel; Lee Yong Hee; Shoelson Steve
     E; White Morris F
CS   Howard Hughes Medical Institute, Joslin Diabetes Center, Harvard Medical
     School, Boston, Massachusetts 02215, USA.
SO   JOURNAL OF BIOLOGICAL CHEMISTRY, (2002 Jan 11) 277 (2) 1531-7.
     Journal code: 2985121R. ISSN: 0021-9258.
CY   United States
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   MEDLINE; Priority Journals
OS   MEDLINE 2002054095
EM   200202
ED   Entered STN: 20020726
     Last Updated on STN: 20020726
AB   Serine phosphorylation of insulin receptor substrate-1 (IRS-1) inhibits
     insulin signal transduction in a variety of cell backgrounds, which might
     contribute to peripheral insulin resistance. However, because of the large
     number of potential phosphorylation sites, the mechanism of inhibition has
     been difficult to determine. One serine residue located near the
     phosphotyrosine-binding (PTB) domain in IRS-1 (Ser(307) in rat IRS-1 or
     Ser(312) in human IRS-1) is phosphorylated via several mechanisms,
     including insulin-stimulated kinases or stress-activated kinases like
     JNK1. During a **yeast tri-hybrid** assay,
     phosphorylation of Ser(307) by JNK1 disrupted the interaction between the
     catalytic domain of the insulin receptor and the PTB domain of IRS-1. In
     32D myeloid progenitor cells, phosphorylation of Ser(307) inhibited

insulin stimulation of the phosphatidylinositol 3-kinase and MAPK cascades. These results suggest that inhibition of PTB domain function in IRS-1 by phosphorylation of Ser(307) (Ser(312) in human IRS-1) might be a general mechanism to regulate insulin signaling.

L3 ANSWER 2 OF 8 BIOTECHNO COPYRIGHT 2002 Elsevier Science B.V.DUPLICATE
AN 2001:32114661 BIOTECHNO
TI Constitutive association of SHP-1 with leukocyte-associated Ig-like receptor-1 in human T cells
AU Sathish J.G.; Johnson K.G.; Fuller K.J.; Leroy F.G.; Meyaard L.; Sims M.J.; Matthews R.J.
CS Dr. R.J. Matthews, Department of Medicine, Tenovus Building, Univ. of Wales College of Medicine, Heath Park, Cardiff CF14 4XX, Wales, United Kingdom.
E-mail: matthewsrj@cardiff.ac.uk
SO Journal of Immunology, (01 FEB 2001), 166/3 (1763-1770), 38 reference(s)
CODEN: JOIMA3 ISSN: 0022-1767
DT Journal; Article
CY United States
LA English
SL English
AB The intracellular Src homology 2 (SH2) domain-containing protein tyrosine phosphatase (SHP-1) is a negative regulator of cell signaling and contributes to the establishment of TCR signaling thresholds in both developing and mature T lymphocytes. Although there is much functional data implicating SHP-1 as a regulator of TCR signaling, the molecular basis for SHP-1 activation in T lymphocytes is poorly defined. A modification of the yeast two-hybrid system was employed to identify in T cells phosphotyrosine-containing proteins capable of binding the SH2 domains of SHP-1. From this **yeast tri-hybrid** screen, the p851.beta. subunit of phosphatidylinositol 3-kinase and the immunoreceptor tyrosine-based inhibitory motif-containing receptors, leukocyte-associated Ig-like receptor-1 (LAIR-1) and programmed death-1 (PD-1), were identified. Coimmunoprecipitation studies demonstrated that the exclusive phosphotyrosine-containing protein associated with SHP-1 in Jurkat T cells under physiological conditions is LAIR-1. Significantly, this interaction is constitutive and was detected only in the membrane-enriched fraction of cell lysates. Ligand engagement of the SH2 domains of SHP-1 is a prerequisite to activation of the enzyme, and, consistent with an association with LAIR-1, SHP-1 was found to be constitutively active in unstimulated Jurkat T cells. Importantly, a constitutive interaction between LAIR-1 and SHP-1 was also detected in human primary T cells. These results illustrate the sustained recruitment and activation of SHP-1 at the plasma membrane of resting human T cells by an inhibitory receptor. We propose that this mechanism may exert a constitutive negative regulatory role upon T cell signaling.

L3 ANSWER 3 OF 8 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 2001:514766 BIOSIS
DN PREV200100514766
TI Dendritic targeting of MAP2-mRNAs in neurons.
AU Kindler, S. (1); Blichenberg, A. (1); Schwanke, B. (1); Rehbein, M. (1); Wege, K. (1); Monshausen, M. (1); Richter, D. (1)
CS (1) Inst for Cell Biochem and Clin Neurobiol, Univ Hospital Eppendorf, Hamburg Germany
SO Society for Neuroscience Abstracts, (2001) Vol. 27, No. 1, pp. 1028. print.
Meeting Info.: 31st Annual Meeting of the Society for Neuroscience San Diego, California, USA November 10-15, 2001
ISSN: 0190-5295.
DT Conference
LA English
SL English
AB The diverse protein composition of distinct subareas in neurons demands

elaborate sorting mechanisms. In addition to intrinsic protein targeting signals, an asymmetric localization and translation of mRNAs contributes to differential protein sorting. In contrast to most neuronal mRNAs that are restricted to somata, transcripts encoding the microtubule-associated protein 2 (MAP2) are found in dendrites. We have identified a cis-acting dendritic targeting element (DTE) in the 3'-untranslated region of MAP2-mRNAs that is capable to impart extrasomatic localization competence on normally non-dendritic reporter mRNAs in primary rat neurons. Along dendritic shafts, mRNAs form granules that may serve as transport units. Utilizing UV cross-linking assays, two 90- and 65-kDa MAP2-RNA trans-acting proteins, MARTA1 and MARTA2, were identified. Both proteins specifically interact with the MAP2-DTE. MARTA1 is the rat orthologue of human KSRP. It contains four KH domains that are thought to mediate RNA-binding. In a **yeast tri-hybrid** screen for additional DTE-binding proteins, a member of a mammalian protein family homologous to the Drosophila RNA-binding protein Staufen was identified. Rat Staufen contains four double-stranded RNA-binding domains and is found in many tissues and brain areas. In rat neurons, Staufen is present in somata and dendrites and accumulates along dendritic microtubules. Two distinct rat brain Staufen isoforms that are encoded by alternatively spliced mRNAs exhibit different in vitro RNA-binding capacities. Binding of MARTA1, MARTA2, and Staufen to the MAP2-DTE may serve to regulate extrasomatic transcript trafficking and translation.

L3 ANSWER 4 OF 8 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 3
AN 2001:349751 BIOSIS
DN PREV200100349751
TI Two rat brain Staufen isoforms differentially bind RNA.
AU Monshausen, Michaela; Putz, Ulrich; Rehbein, Monika; Schweizer, Michaela; DesGroseillers, Luc; Kuhl, Dietmar; Richter, Dietmar; Kindler, Stefan (1)
CS (1) Institute for Cell Biochemistry and Clinical Neurobiology, University of Hamburg, D-20246, Hamburg: kindler@uke.uni-hamburg.de Germany
SO Journal of Neurochemistry, (January, 2001) Vol. 76, No. 1, pp. 155-165. print.
ISSN: 0022-3042.
DT Article
LA English
SL English
AB In neurones, a limited of mRNAs is found in dendrites, including transcripts encoding the microtubule-associated protein 2 (MAP2). Recently, we identified a cis-acting dendritic targeting element (DTE) in MAP2 mRNAs. Here we used the **yeast tri-hybrid** system to identify potential trans-acting RNA-binding factors of the DTE. A cDNA clone was isolated that encodes a member of a mammalian protein family that is highly homologous to the Drosophila RNA-binding protein Staufen. Mammalian Staufen appears to be expressed in most tissues and brain areas. Two distinct rat brain Staufen isoforms, rStau+16 and rStau-16, are encoded by alternatively spliced mRNAs. Both isoforms contain four double-stranded RNA-binding domains (dsRBD). In the larger rStau+16 isoform, six additional amino acids are inserted in the second dsRBD. Although both isoforms interacted with the MAP2-DTE and various additional RNA fragments in an in vitro north-western assay, rStau-16 exhibited a stronger signal of bound radioactively labelled RNAs as compared with rStau+16. Using an antibody directed against mammalian Staufen, the protein was detected in somata and dendrites of neurones of the adult rat hippocampus and cerebral cortex. Ultrastructural studies revealed that in dendrites, rat Staufen accumulates along microtubules. Thus in neurones, rat Staufen may serve to link RNAs to the dendritic microtubular cytoskeleton and may thereby regulate their subcellular localization.

L3 ANSWER 5 OF 8 AGRICOLA DUPLICATE 4
AN 2001:80163 AGRICOLA
DN IND23232697

TI NIMIN-1, NIMIN-2 and NIMIN-3, members of a novel family of proteins from Arabidopsis that interact with NPR1/NIM1, a key regulator of systemic acquired resistance in plants.
AU Weigel, R.R.; Bauscher, C.; Pfitzner, A.J.P.; Pfitzner, U.M.
AV DNAL (QK710.P62)
SO Plant molecular biology, May 2001. Vol. 46, No. 2. p. 143-160
Publisher: Dordrecht : Kluwer Academic Publishers.
CODEN: PMBIDB; ISSN: 0167-4412
NTE Includes references
CY Netherlands
DT Article
FS Non-U.S. Imprint other than FAO
LA English
AB NPR1/NIM1 is a key regulator of systemic acquired resistance (SAR) in Arabidopsis. Using the yeast two-hybrid system, we have identified three novel genes, NIMIN-1, NIMIN-2 and NIMIN-3 (NIMIN for NIM1-interacting) that encode structurally related proteins interacting physically with NPR1/NIM1. NIMIN-1 and NIMIN-2 both bind strongly to NPR1/NIM1 via a common binding motif interacting with the C-terminal moiety of NPR1/NIM1, whereas NIMIN-3 interacts with NPR1/NIM1 via the N-terminal part of NPR1/NIM1. In addition, NIMIN-1, NIMIN-2, and NIMIN-3 are able to interact via NPR1/NIM1 with basic leucine zipper transcription factors of the TGA family in a **yeast tri-hybrid** system. A mutant protein of NPR1/NIM1, npr1-2, which has been shown to be severely impaired in induction of SAR gene expression, failed to bind the NIMIN proteins. The NIMIN genes are expressed in Arabidopsis plants in response to SAR-inducing treatments, and the NIMIN proteins, like NPR1/NIM1, carry functional nuclear localization signals as revealed by expression of fusion proteins in yeast and in transgenic plants. Taken together, these data indicate that the NIMIN proteins, via physical interaction with NPR1/NIM1, are part of the signal transduction pathway leading to SAR gene expression in Arabidopsis.

L3 ANSWER 6 OF 8 CAPLUS COPYRIGHT 2002 ACS
AN 2001:57631 CAPLUS
DN 135:267809
TI RNA-protein interactions reconstituted by a tri-hybrid system
AU Putz, Ulrich; Kremerskothen, Joachim; Skehel, Paul; Kuhl, Dietmar
CS Zentrum fur Molekulare Neurobiologie Hamburg, University of Hamburg, Hamburg, Germany
SO Yeast Hybrid Technologies (2000), 207-219. Editor(s): Zhu, Li; Hannon, Gregory J. Publisher: Eaton Publishing Co., Natick, Mass.
CODEN: 69AWKB
DT Conference
LA English
AB A modification of the yeast two-hybrid system for the in vivo reconstruction of specific RNA-protein interactions is described. In this trihybrid system, the DNA binding and transcription activation domains of the yeast transcriptional activator GAL4 are brought together via the interaction of recombinant fusion proteins with a recombinant RNA. The three component mols. used in the trihybrid system are the RevM10 protein fused to the DNA-binding domain of GAL4, an RNA-hybrid contg. the RRE sequence fused to a target RNA, and a second protein hybrid comprised of the activation domain of GAL4 fused to any protein of interest or to proteins expressed from a library of cDNAs. Each hybrid protein and the hybrid RNA is expressed in yeast cells that are under the control of an independent promoter and termination sequences. Upon productive interaction of the three hybrid mols. a functional GAL4 transcription factor is reconstituted. The activity of this transcription factor is then used to report the RNA-protein interaction. It may be used to detect specific RNA-binding proteins or target RNAs from a library of cDNAs, or to analyze the structural specificity of identified RNA-protein interactions. One of the major advantages of the method is that a multiplicity of proteins or RNAs can be tested simultaneously for the

interaction with an RNA or protein of interest. The method is amenable to the anal. of a wide variety of ribonucleoprotein complexes. However, a tri-hybrid interaction does not ascertain a physiol. function or relevance.

RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 7 OF 8 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 2001:289123 BIOSIS
DN PREV200100289123
TI Molecular cloning and characterization of interleukin 13 receptor binding protein.
AU Murata, Takashi (1); Kurokawa, Kenji (1); Sasaki, Atsuo; Yoshimura, Akihiko; Puri, Raj K.; Kobayashi, Nobuyuki (1)
CS (1) Pharm. Sci., Nagasaki Univ., Nagasaki Japan
SO Blood, (November 16, 2000) Vol. 96, No. 11 Part 2, pp. 140b. print.
Meeting Info.: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000 American Society of Hematology
. ISSN: 0006-4971.
DT Conference
LA English
SL English
AB Interleukin 13 (IL-13) has been shown to play a critical role in the allergic diseases and bronchial asthma. However, signal transduction mechanisms for IL-13 receptor complex is still completely not clear. To investigate its signal transduction pathways, we have cloned new IL-13 Ralpha' binding protein by **yeast tri-hybrid** system and designated it interleukin 13 receptor binding protein 1 (IL-13RBP1). IL-13RBP1 cDNA is 2370 bp in length with open reading frame predicted to encode a protein of 625 amino acids. MOTIF search analysis revealed that IL-13RBP1 cDNA contains a myosin heavy chain like sequence in the N terminal end, nuclear localization signal in the middle part and coiled-coil region in C terminal end. We next examined mRNA expression in human tissues by Northern analysis and found that two different sizes (4.4 and 2.4 kb) of IL13RBP1 transcripts were present in most tissues. In addition, testis contained an additional 3 types of transcripts of apprx2.7 kb. Database searches utilizing BLAST and FASTA programs failed to identify any mammalian proteins having significant sequence similarities to IL13RBP1. However, C. elegans and D. melanogaster proteins of unknown function share apprx20% similarity to IL-13RBP1. IL-13RBP1 may provide a novel mechanism in IL-13R signal transduction pathways.

L3 ANSWER 8 OF 8 JICST-EPlus COPYRIGHT 2002 JST
AN 1000050313 JICST-EPlus
TI Analysis of tyrosine kinase signaling by **yeast tri-hybrid** system.
AU SASAKI ATSUO; ENDO TAKAHO; YOSHIMURA AKIHIKO
CS Kurume Univ., Inst. Life Sci., JPN
SO Jikken Igaku (Experimental Medicine), (1999) vol. 17, no. 19, pp. 2579-2583. Journal Code: Y0568A (Fig. 3, Tbl. 1, Ref. 4)
ISSN: 0288-5514
CY Japan
DT Journal; Commentary
LA Japanese
STA New

=>
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<------User Break------>

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  23 FILES SEARCHED...
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  41 FILES SEARCHED...
  47 FILES SEARCHED...
  60 FILES SEARCHED...
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L4       113844 (PROTEIN PROTEIN INTERACTION)

=> s l4 (4A) (intact cell)
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  13 FILES SEARCHED...
  29 FILES SEARCHED...
  41 FILES SEARCHED...
  53 FILES SEARCHED...
  64 FILES SEARCHED...
L5           14 L4 (4A) (INTACT CELL)

=> s l4 (4A) coexpression
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L6            2 L4 (4A) COEXPRESSION

=> s l5 or l6
  58 FILES SEARCHED...
L7           15 L5 OR L6

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ENTER L# LIST OR (END):l7
DUPLICATE IS NOT AVAILABLE IN 'ADISINSIGHT, ADISNEWS, BIOCOMMERCE, DGENE,
DRUGLAUNCH, DRUGMONOG2, DRUGUPDATES, FEDRIP, FOREGE, GENBANK, KOSMET,
MEDICONF, PHAR, PHARMAML, SYNTHLINE, CHEMLIST, HSDB, MSDS-CCOHS, MSDS-OHS,
RTECS, CONF, EVENTLINE, IMSDRUGCONF, DIOGENES, INVESTEXT, USAN, FORIS, FORKAT,
UFORDAT, AQUIRE'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
DUPLICATE PREFERENCE IS 'BIOSIS, BIOTECHNO, CANCERLIT, CAPLUS, EMBASE, ESBIOBASE,
MEDLINE, SCISEARCH, USPATFULL'
KEEP DUPLICATES FROM MORE THAN ONE FILE?  Y/(N):n
PROCESSING COMPLETED FOR L7
L8            8 DUPLICATE REMOVE L7 (7 DUPLICATES REMOVED)

=> d l8 1-8 bib ab

L8   ANSWER 1 OF 8  USPATFULL
AN     2002:272801  USPATFULL
TI     Compositions and methods for the therapy and diagnosis of colon cancer
IN     Stolk, John A., Bothell, WA, UNITED STATES
       Xu, Jiangchun, Bellevue, WA, UNITED STATES
       Chenault, Ruth A., Seattle, WA, UNITED STATES
       Meagher, Madeleine Joy, Seattle, WA, UNITED STATES
PA     Corixa Corporation, Seattle, WA, UNITED STATES, 98104 (U.S. corporation)
PI     US 2002150922      A1   20021017
AI     US 2001-998598     A1   20011116 (9)
PRAI   US 2001-304037P     20010710 (60)
       US 2001-279670P     20010328 (60)
       US 2001-267011P     20010206 (60)
       US 2000-252222P     20001120 (60)
DT     Utility
FS     APPLICATION
LREP   SEED INTELLECTUAL PROPERTY LAW GROUP PLLC, 701 FIFTH AVE, SUITE 6300,
       SEATTLE, WA, 98104-7092
CLMN   Number of Claims: 17
```

ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 9233
AB Compositions and methods for the therapy and diagnosis of cancer, particularly colon cancer, are disclosed. Illustrative compositions comprise one or more colon tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly colon cancer.

L8 ANSWER 2 OF 8 USPATFULL
AN 2002:243051 USPATFULL
TI Compositions and methods for the therapy and diagnosis of ovarian cancer
IN Algate, Paul A., Issaquah, WA, UNITED STATES
Jones, Robert, Seattle, WA, UNITED STATES
Harlocker, Susan L., Seattle, WA, UNITED STATES
PA Corixa Corporation, Seattle, WA, UNITED STATES, 98104 (U.S. corporation)
PI US 2002132237 A1 20020919
AI US 2001-867701 A1 20010529 (9)
PRAI US 2000-207484P 20000526 (60)
DT Utility
FS APPLICATION
LREP SEED INTELLECTUAL PROPERTY LAW GROUP PLLC, 701 FIFTH AVE, SUITE 6300, SEATTLE, WA, 98104-7092
CLMN Number of Claims: 11
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 25718
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Compositions and methods for the therapy and diagnosis of cancer, particularly ovarian cancer, are disclosed. Illustrative compositions comprise one or more ovarian tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly ovarian cancer.

L8 ANSWER 3 OF 8 CAPLUS COPYRIGHT 2002 ACS
AN 2002:75436 CAPLUS
DN 137:197622
TI Identification of associated proteins by coimmunoprecipitation
AU Adams, Peter D.; Seeholzer, Steven; Ohh, Michael
CS Fox Chase Cancer Center, Philadelphia, PA, 19111, USA
SO Protein-Protein Interactions (2002), 59-74. Editor(s): Golemis, Erica. Publisher: Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N. Y. CODEN: 69CFYI; ISBN: 0-87969-628-1
DT Conference; General Review
LA English
AB A review describes the co-immunopptn. technique for the identification of assocd. proteins, as well as the controls that should be performed to guarantee that a coimmunopptg. protein is truly an in in-vivo-assocd. protein. Co-immunopptn. can also be used to search for novel proteins that interact with a known protein of interest. It is a powerful way to identify physiol. **protein-protein interactions** that exist within the **intact cell**. However, it can be relatively laborious and time-consuming, and often requires a very large no. of cultured cells. In the co-immunopptn. method, the cells are harvested and lysed under conditions that preserve protein-protein interactions, a protein of interest is specifically immunopptd. from the cell exts., and the immunoppts. are then fractionated by PAGE. Co-immunopptn. of a protein of known identity is most commonly detected by

Western blotting with an antibody directed against that protein.
RE.CNT 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 4 OF 8 USPATFULL
AN 2001:219031 USPATFULL
TI Mapping molecular interactions in plants with protein fragments complementation assays
IN Brisson, Normand, Montreal, Canada
Michnick, Stephen William Watson, Westmount, Canada
PI US 2001047526 A1 20011129
AI US 2001-851084 A1 20010509 (9)
PRAI US 2000-203937P 20000512 (60)
DT Utility
FS APPLICATION
LREP Isaac A. Angres, Suite 301, 2001 Jefferson Davis Highway, Arlington, VA, 22202
CLMN Number of Claims: 26
ECL Exemplary Claim: 1
DRWN 10 Drawing Page(s)
LN.CNT 1297
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention describes a method of expressing PCA interacting partners in plant material comprising: (A) transforming said material with: (1) a first construct coding for a first fusion product comprising (a) a first fragment of a first molecule whose fragments can exhibit a detectable activity when associated and (b) a first protein-protein interacting domain; and (2) a second construct coding for a second fusion product comprising (a) a second fragment of said first molecule and (b) a second protein-protein interacting domain that can bind (1)(b); (B) culturing said material under conditions allowing expression of said PCA interacting partners; and (C) detecting said activity.

L8 ANSWER 5 OF 8 CAPLUS COPYRIGHT 2002 ACS
AN 2001:164249 CAPLUS
DN 134:337720
TI Dissecting the Interaction Network of Multiprotein Complexes by Pairwise Coexpression of Subunits in E. coli
AU Fribourg, Sebastien; Romier, Christophe; Werten, Sebastiaan; Gangloff, Yann-Gael; Poterszman, Arnaud; Moras, Dino
CS Institut de Genetique et de Biologie Cellulaire et Moleculaire, CNRS/INSERM/ULP, College de France, C. U. de Strasbourg, 67404, Fr.
SO Journal of Molecular Biology (2001), 306(2), 363-373
CODEN: JMOBAK; ISSN: 0022-2836
PB Academic Press
DT Journal
LA English
AB Using the human basal transcription factors TFIID and TFIIH as examples, we show that pairwise coexpression of polypeptides in Escherichia coli can be used as a tool for the identification of specifically interacting subunits within multiprotein complexes. We find that coexpression of appropriate combinations generally leads to an increase in the soly. and stability of the polypeptides involved, which means that large amts. of the resulting complexes can immediately be obtained for subsequent biochem. and structural anal. Furthermore, we demonstrate that the solubilization and/or the proper folding of a protein by its natural partner can be used as a monitor for deletion mapping to det. precise interaction domains. Coexpression can be used as an alternative or complementary approach to conventional techniques for interaction studies such as yeast two-hybrid anal., GST pulldown and immunopptn. (c) 2001 Academic Press.
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 6 OF 8 CAPLUS COPYRIGHT 2002 ACS
AN 2000:538587 CAPLUS
DN 134:174936
TI Detection of **protein-protein interaction** in **intact cells** by Protein-fragment Complementation Assay (PCA)
AU Inoue, Kaoru; Koide, Hiroshi
CS Faculty of Bioscience and Biotechnology, Tokyo Institute of Technology, Japan
SO Jikken Igaku (2000), 18(10), 1417-1419
CODEN: JIIGEF; ISSN: 0288-5514
PB Yodosha
DT Journal; General Review
LA Japanese
AB A review with 5 refs. on the protein fragment complementation assay (PCA) method for study in vivo protein interaction. The principle, prepn., and protocol of the PCA method were given. .beta.-Galactosidase is used to study protein interaction on cell membrane by the PCA method, and improvement of the method with tetrahydrofolate dehydrogenase and ubiquinone discussed.

L8 ANSWER 7 OF 8 CAPLUS COPYRIGHT 2002 ACS
AN 2000:850029 CAPLUS
DN 134:143505
TI Detection of protein-protein interactions by protein fragment complementation studies
AU Michnick, Stephen W.; Remy, Ingrid; Campbell-Valois, Francois-X.; Vallee-Belisle, Alexis; Pelletier, Joelle N.
CS Departement de Biochimie, Universite de Montreal, Montreal, QC, H3C 3J7, Can.
SO Methods in Enzymology (2000), 328(Applications of Chimeric Genes and Hybrid Proteins, Pt. C), 208-230
CODEN: MENZAU; ISSN: 0076-6879
PB Academic Press
DT Journal
LA English
AB A general strategy has been developed for detecting **protein-protein interactions** in **intact cells** based on protein fragment complementation assays (PCAs). The gene coding of an enzyme is rationally dissected into two pieces. Fusion proteins are constructed with two proteins that are thought to bind to each other, fused to either of the two probe fragments. Folding of the probe protein from its fragments is initiated by the binding of the test proteins to each other, and is detected as reconstitution of enzyme activity. The basic concept of PCAs and how they are designed are presented, with particular attention to the first system developed, based on murine dihydrofolate reductase. Several applications of the assay are presented, including a simple, large-scale library-vs.-library screening strategy in Escherichia coli. The implementation of mammalian assays is discussed, including applications to the quant. detection of induced protein interactions and allosteric transitions, in intact cells. Finally, the generality of the PCA strategy is demonstrated with examples of assays which have been designed on the basis of other enzymes including glycinamide ribonucleotide transformylase, aminoglycoside kinase, and hygromycin B kinase. (c) 2000 Academic Press.

L8 ANSWER 8 OF 8 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 1
AN 1997:199076 BIOSIS
DN PREV199799498279
TI 5-Iodonaphthyl-1-azide labeling of plasma membrane proteins adjacent to specific sites via energy transfer.
AU Meiklejohn, Bruce I.; Rahman, Noorulhuda A.; Roess, Deborah A.; Barisas, B. George (1)
CS (1) Dep. Chem. Physiol., Colorado State Univ., Ft. Collins, CO 80523 USA

SO Biochimica et Biophysica Acta, (1997) Vol. 1324, No. 2, pp. 320-332.
ISSN: 0006-3002.
DT Article
LA English
AB We have examined conditions optimal for 5-iodonaphthyl-1-azide (INA-4) labeling of membrane proteins proximal to known membrane sites. Membrane-bound INA can be indirectly activated by energy transfer from visible chromophores. We demonstrate that the efficiency of this sensitized activation is enhanced by use of triplet-forming chromophores such as eosin and by deoxygenation. Variation of sensitized activation efficiency with INA concentration indicates that the critical distance for eosin-INA energy transfer in solution is 8-14 ANG . We suggest that photosensitization occurs through triplet exchange and present an improved labeling protocol based on these findings. This protocol was used to examine whether different accessory proteins are associated with isolated and crosslinked Type I Fc-epsilon receptors on 2H3 rat basophilic leukemia cells. 2H3 cells were incubated with eosin-conjugated IgE and irradiated at 514 nm yielding (125I)INA derivatized peptides at 53, 38, 34, and 29 kDa. Crosslinking IgE with mouse anti-rat IgE prior to irradiation labeled three additional proteins at 60, 54, and 43 kDa. These results demonstrate the utility of sensitized INA labeling in characterizing **protein -protein interactions** in membranes of **intact cells** and indicate the importance of considering photophysical factors when selecting sensitizers and reaction conditions. We discuss estimation of the size of the membrane region surrounding a sensitizing chromophore within which INA labeling of membrane proteins occurs.

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nested terms that are not separated by a logical operator.

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UNMATCHED LEFT PARENTHESIS 'W) (TRANSFECTI'
The number of right parentheses in a query must be equal to the
number of left parentheses.

=> s sh2 (w) domain (w) (transfection or expression)
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68 FILES SEARCHED...
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DRUGLAUNCH, DRUGMONOG2, DRUGUPDATES, FEDRIP, FOREGE, GENBANK, KOSMET, MEDICONF, PHAR, PHARMAML, SYNTHLINE, CHEMLIST, HSDB, MSDS-CCOHS, MSDS-OHS, RTECS, CONF, EVENTLINE, IMSDRUGCONF, DIOGENES, INVESTEXT, USAN, FORIS, FORKAT, UFORDAT, AQUIRE'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
DUPLICATE PREFERENCE IS 'BIOSIS, BIOTECHNO, CABA, CANCERLIT, CAPLUS, DGENE, EMBASE, ESBIOBASE, LIFESCI, MEDLINE, PASCAL, SCISEARCH, USPATFULL'
KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n
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L11 17 DUPLICATE REMOVE L9 (23 DUPLICATES REMOVED)

=> d l11 1-17 bib ab

L11 ANSWER 1 OF 17 CAPLUS COPYRIGHT 2002 ACS
AN 2002:454772 CAPLUS
TI Expression of a mutated form of the p85.alpha. regulatory subunit of phosphatidylinositol 3-kinase in a Hodgkin's lymphoma-derived cell line (CO)
AU Jucker, M.; Sudel, K.; Horn, S.; Sickel, M.; Wegner, W.; Fiedler, W.; Feldman, R. A.
CS Institut fur Medizinische Biochemie und Molekularbiologie, Universitatsklinikum Hamburg-Eppendorf, Hamburg, Germany
SO Leukemia (2002), 16(5), 894-901
CODEN: LEUKED; ISSN: 0887-6924
PB Nature Publishing Group
DT Journal
LA English
AB Phosphatidylinositol (PI) 3-kinase plays an important role in a variety of biol. processes, including proliferation and apoptosis. PI3-kinase is a heterodimer consisting of an 85 kDa adapter protein (p85) contg. one SH3 domain and two SH2 domains and a 110 kDa catalytic subunit (p110). Recently an oncogenic form of p85 named p65-PI3K lacking the C-terminal SH2 domain has been cloned from an irradn.-induced murine thymic lymphoma and transgenic mice expressing p65-PI3K in T lymphocytes develop a lymphoproliferative disorder. Here the authors describe the cloning of a C-terminal truncated form of p85 expressed in a human lymphoma cell line (CO) with a T cell phenotype derived from a patient with Hodgkin's disease. As a result of a frame-shift mutation at amino acid 636, p76 is lacking most of the C-terminal SH2 domain, but contains the inter-SH2 domain and is assocd. with an active form of PI3-kinase. A PI3-kinase-dependent constitutive activation of Akt was detected in CO cells which was only partially reduced after serum starvation. Treatment of CO cells with the PI3-kinase inhibitor wortmannin resulted in a concn.-dependent inhibition of cell proliferation assocd. with an increased no. of apoptotic cells. This is the first detection of a mutated form of the p85 subunit of PI3-kinase in human hematopoietic cells further underlining a potential role of PI3-kinase/Akt signaling in human leukemogenesis.
RE.CNT 64 THERE ARE 64 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 2 OF 17 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 2001:101799 BIOSIS
DN PREV200100101799
TI Role of the APS adapter protein in insulin receptor signalling.
AU Ahmed, Z. (1); Smith, B. J. (1); Wylie, P. (1); Pillay, T. S. (1)
CS (1) Institute of Cell Signalling and School of Biomedical Sciences, Queen's Medical Centre, University of Nottingham, Nottingham, NG7 2UH UK
SO Biochemical Society Transactions, (October, 2000) Vol. 28, No. 5, pp. A270. print.
Meeting Info.: 18th International Congress of Biochemistry and Molecular Biology Birmingham, UK July 16-20, 2000
ISSN: 0300-5127.
DT Conference

LA English
SL English

L11 ANSWER 3 OF 17 CAPLUS COPYRIGHT 2002 ACS
AN 1999:219732 CAPLUS
DN 130:247852
TI Expression-cloning method for identifying target proteins for eukaryotic tyrosine kinases and novel target proteins
IN Schlessinger, Joseph; Skolnik, Edward Y.; Margolis, Benjamin L.; App, Harald
PA New York University Medical Center, USA
SO U.S., 137 pp., Cont.-in-part of U.S. Ser. No. 208,227, abandoned.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 5889150	A	19990330	US 1994-252820	19940602
	US 5434064	A	19950718	US 1992-906349	19920630
	US 5618691	A	19970408	US 1993-167035	19931216
	US 6391584	B1	20020521	US 1999-280598	19990329
PRAI	US 1991-643237	B2	19910118		
	US 1992-906349	A2	19920630		
	US 1993-167035	A2	19931216		
	US 1994-208227	B2	19940310		
	US 1994-208887	A2	19940311		
	US 1994-252820	A3	19940602		

AB A novel method, based on direct expression cloning, for identifying target proteins capable of binding to or serving as substrates for receptor or cytoplasmic tyrosine kinases. In essence, expression libraries are screened with ligands for the kinase or with substrate-binding fragments of kinases. The present invention also relates to novel proteins identified using this method, and to methods for identifying compds. that disrupt the interaction of such novel proteins with the receptor or cytoplasmic tyrosine kinases. A phosphorylated C-terminal tail of human epidermal growth factor receptor was used to screen expression cDNA libraries from a no. of tissues. A cDNA from a brainstem library found by this method encoded a protein contg. SH2 and SH3 domains. The mRNA was present in brain, heart, spleen, and liver.
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 4 OF 17 USPATFULL
AN 1999:141669 USPATFULL
TI Human syk
IN Brugge, Joan, Concord, MA, United States
Morganstern, Jay, Boston, MA, United States
Shiue, Lily, Cambridge, MA, United States
Zydowsky, Lynne, Cambridge, MA, United States
Zoller, Mark, Weston, MA, United States
Pawson, Anthony, Toronto, Canada
PA Ariad Pharmaceuticals, Inc., Cambridge, MA, United States (U.S. corporation)
PI US 5981262 19991109
WO 9425565 19941110
AI US 1996-596319 19960131 (8)
WO 1994-US4540 19940425
19960131 PCT 371 date
19960131 PCT 102(e) date
RLI Continuation-in-part of Ser. No. US 1993-52560, filed on 23 Apr 1993, now abandoned
DT Utility
FS Granted

EXNAM Primary Examiner: Achutamurthy, Ponnathapura; Assistant Examiner: Saidha, Tekchand
LREP Berstein, David L., Hausdorff, Sharon F., Clauss, Isabelle M.
CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN 2 Drawing Figure(s); 4 Drawing Page(s)
LN.CNT 1798
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The molecular cloning of humansyk DNA, compositions containing same and uses thereof are disclosed.

L11 ANSWER 5 OF 17 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1999:91097 BIOSIS
DN PREV199900091097
TI Characterization and binding specificity of the monomeric STAT3-SH2 domain.
AU Haan, Serge; Hemmann, Ulrike; Hassiepen, Ulrich; Schaper, Fred; Schneider-Mergener, Jens; Wollmer, Axel; Heinrich, Peter C. (1); Groetzinger, Joachim
CS (1) Institut fuer Biochemie, RWTH-Aachen, Pauwelsstrasse 30, D-52074 Aachen Germany
SO Journal of Biological Chemistry, (Jan. 15, 1999) Vol. 274, No. 3, pp. 1342-1348.
ISSN: 0021-9258.
DT Article
LA English
AB Signal transducers and activators of transcription (STATs) are important mediators of cytokine signal transduction. STAT factors are recruited to phosphotyrosine-containing motifs of activated receptor chains via their SH2 domains. The subsequent tyrosine phosphorylation of the STATs leads to their dissociation from the receptor, dimerization, and translocation to the nucleus. Here we describe the expression, purification, and refolding of the STAT3-SH2 domain. Proper folding of the isolated protein was proven by circular dichroism and fluorescence spectroscopy. The STAT3-SH2 domain undergoes a conformational change upon dimerization. Using an enzyme-linked immunosorbent assay we demonstrate that the monomeric domain binds to specific phosphotyrosine peptides. The specificity of binding to phosphotyrosine peptides was assayed with the tyrosine motif encompassing Tyr705 of STAT3 and with all tyrosine motifs present in the cytoplasmic tail of the signal transducer gp130.

L11 ANSWER 6 OF 17 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1999:288723 BIOSIS
DN PREV199900288723
TI Potent inhibitory ligands of the GRB2 SH2 domain from recombinant peptide libraries.
AU Hart, Charles P. (1); Martin, Jennifer E.; Reed, Margaret A.; Keval, Aftab A.; Pustelnik, Matthew J.; Northrop, Jeffrey P.; Patel, Dinesh V.; Grove, J. Russell
CS (1) 3410 Central Expressway, Santa Clara, CA, 95051-0703 USA
SO Cellular Signalling, (June, 1999) Vol. 11, No. 6, pp. 453-464.
ISSN: 0898-6568.
DT Article
LA English
SL English
AB We cloned and expressed the SH2 domain of human GRB2 as glutathione S-transferase and maltose binding protein fusion proteins. We screened three phagemid-based fd pVIII-protein phage display libraries against SH2 domain fusion proteins. Sequence analysis of the peptide extensions yielded a variety of related peptides. By examining the ability of the phage clones to bind other SH2 domains, we demonstrated that the phage were specific for the SH2 domain of GRB2. Based on the sequence motif identified in the "random" library screening experiment, we also built and screened a phage display library based on a Tyr-X-Asn motif

(X5-Tyr-X-Asn-X8). To examine the affinity of the phage derived peptides for GRB2, we set up a radioligand competition binding assay based on immobilized GRB2 and radiolabelled autophosphorylated EGFR ICD as the radioligand. Results obtained with peptide competitors derived from the phage sequences demonstrated that nonphosphotyrosine-containing peptides identified with the phage display technology had an affinity for the receptor similar to tyrosine-phosphorylated peptides derived from the EGFR natural substrate. Interestingly, when the phage display peptides were then phosphorylated on tyrosine, their affinity for GRB2 increased dramatically. We also demonstrated the ability of the peptides to block the binding of the GRB2 SH2 domain to EGFR in a mammalian cell-based binding assay.

L11 ANSWER 7 OF 17 USPATFULL
AN 1998:88934 USPATFULL
TI Modified SH2 domains
IN Waksman, Gabriel, University City, MO, United States
Shaw, Andrey, St. Louis, MO, United States
PA Washington University School of Medicine, St. Louis, MO, United States (U.S. corporation)
PI US 5786454 19980728
AI US 1994-308086 19940916 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Allen, Marianne P.; Assistant Examiner: Gucker, Stephen
LREP Arnall Golden & Gregory, LLP
CLMN Number of Claims: 19
ECL Exemplary Claim: 1
DRWN 15 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 952
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Modified SH2 domains of intracellular proteins and methods of use, wherein the SH2 domains are modified to include an altered binding site for a signal transduction protein. The binding site is altered to either change the specificity of the SH2 domain for a signal transduction protein that is not the natural ligand or to include a reactive group, such as a reactive amino acid, that reacts with a phosphorylated amino acid of the signal transduction protein. The modified SH2 domains are useful as research tools or in methods for inactivating or inhibiting signal transduction proteins, especially those that contribute to disease or disorders such as cancer or for targeting specific SH2 domains for diagnostics.

L11 ANSWER 8 OF 17 CAPLUS COPYRIGHT 2002 ACS
AN 1997:308982 CAPLUS
DN 127:47878
TI Expression of mutated Nck SH2/SH3 adaptor respecifies mesodermal cell fate in Xenopus laevis development
AU Tanaka, Masamitsu; Lu, Wange; Gupta, Ruchika; Mayer, Bruce J.
CS Howard Hughes Medical Institute, Children's Hospital, and Department of Microbiology and Molecular Genetics, Harvard Medical School, Boston, MA, 02115, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1997), 94(9), 4493-4498
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Nck is a widely expressed SH2/SH3 adaptor protein contg. one SH2 and three SH3 domains. Although Nck is assumed to mediate the formation of protein-protein complexes during signaling, little is currently known about its specific function. The authors have constructed a series of Nck SH3 and SH2 domain mutants, expressed them in Xenopus laevis embryos, and

monitored injected embryos for developmental abnormalities. This approach allows correlation of developmental phenotypes with the presence or absence of specific Nck protein-binding domains. The authors show that microinjection of RNA-encoding Nck with an inactivating mutation in the third SH3 domain (NckK229) into dorsal blastomeres of early embryos caused anterior truncation with high frequency, and membrane localization of both the first and second SH3 domains together was sufficient to induce this anterior-truncation phenotype. Mol. marker anal. of explants revealed that the expression of NckK229 ventralized dorsal mesoderm. Lineage tracing expts. demonstrated that the expression of Nck K229 in dorsal blastomeres affected the migratory properties of mesoderm cells in gastrulation and led to the adoption of a more posterior fate. These data suggest that protein(s) that bind the first and second SH3 domains of Nck can affect the response to signals that establish dorsoventral patterning, and that protein(s) that bind the third SH3 domain antagonize the ventralizing effect of the first two SH3 domains.

L11 ANSWER 9 OF 17 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 1
AN 1997:411958 BIOSIS
DN PREV199799704001
TI The G-12 coupled thrombin receptor stimulates mitogenesis through the Shc SH2 domain.
AU Collins, Lila R.; Ricketts, William A.; Olefsky, Jerrold M.; Brown, Joan Heller (1)
CS (1) Dep. Pharmacol., Univ. California, San Diego, La Jolla, CA 92093 USA
SO Oncogene, (1997) Vol. 15, No. 5, pp. 595-600.
ISSN: 0950-9232.
DT Article
LA English
AB Our previous studies in 1321N1 astrocytoma cells demonstrate that thrombin stimulates Ras-dependent mitogenesis through the pertussis toxin insensitive G protein G-12. While the direct effectors of G-12 are unknown, G-alpha-12 can transform fibroblasts, utilize Ras and Rac dependent signaling pathways and stimulate GTP loading of Ras. Here we have examined the role of the Shc adaptor protein in mitogenic signaling by the thrombin receptor in 1321N1 cells. As has been reported in other systems, thrombin stimulation results in tyrosine phosphorylation of Shc in 1321N1 cells. We also show that transient expression of G-alpha-12 results in tyrosine phosphorylation of She, thereby identifying Shc as the most proximal G-12 effector to date. In addition, we demonstrate by microinjection that thrombin stimulated mitogenesis requires Shc and occurs specifically through the Shc **SH2 domain**.
Expression of the SH2 domain of Shc also inhibits G-alpha-12 mediated induction of an AP-1 dependent reporter gene demonstrating that G-12 utilizes Shc to propagate downstream signals. Our data indicate that Shc is essential for stimulation of Ras dependent mitogenesis and gene expression by the G-12 coupled thrombin receptor.

L11 ANSWER 10 OF 17 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1998:67173 BIOSIS
DN PREV199800067173
TI Expression of the Abl SH2 domain activates the c-Abl tyrosine kinase and induces morphological transformation.
AU Ma, G.; Wu, Y.; Liu, J.; Arlinghaus, R. B.
CS Dep. Molecular Pathology, Univ. Texas M.D. Anderson Cancer Cent., Houston, TX USA
SO Blood, (Nov. 15, 1997) Vol. 90, No. 10 SUPPL. 1 PART 1, pp. 196A.
Meeting Info.: 39th Annual Meeting of the American Society of Hematology San Diego, California, USA December 5-9, 1997 The American Society of Hematology
. ISSN: 0006-4971.
DT Conference
LA English

L11 ANSWER 11 OF 17 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 2
AN 1996:457457 BIOSIS
DN PREV199699179813
TI PI 3-kinase activation in BCR/abl-transformed hematopoietic cells does not require interaction of p85 SH2 domains with p210 BCR/abl.
AU Jain, Suresh K.; Susa, Mira; Keeler, Marilyn L.; Carlesso, Nadia; Druker, Brian; Varticovski, Lyuba (1)
CS (1) Dep. Biomed. Res., St. Elizabeth's Med. Cent., Tufts USM, 736 Cambridge St., Boston, MA 02135 USA
SO Blood, (1996) Vol. 88, No. 5, pp. 1542-1550.
ISSN: 0006-4971.
DT Article
LA English
AB BCR/abl is a chimeric oncogene implicated in the pathogenesis of human chronic myelogenous leukemia. Expression of the BCR/abl gene induces hematologic malignancies in transgenic mice and transformation of interleukin-3-dependent hematopoietic cells. The mechanism of BCR/abl-mediated transformation of hematopoietic cells is poorly understood and involves activation of at least two signaling pathways, p21-ras and PI 3-kinase. Here we report that PI 3,4-P-2 and PI 3,4,5-P-3, the enzymatic products of PI 3-kinase, accumulate in metabolically labeled transformed hematopoietic cells, in contrast to our previous report on the lack of accumulation of PI 3-kinase products in nontransformed NIH 3T3 fibroblasts that express p210 BCR/abl. Transformed cells also have increased PI 3-kinase activity in total cell extracts and membrane fractions. Activation of PI 3-kinase occurs by occupancy of SH2 domains of PI 3-kinase regulatory subunit, p85, by phosphorylated YXXM motifs. Therefore, we investigated whether BCR/abl binds to p85 and whether this binding is mediated by interaction of p85 SH2 domains with YXXM motif of BCR/abl. Association of p210 BCR/abl with p85 in immune complexes and with p85 SH2 domains was evident in hematopoietic cells that express the wt p210 BCR/abl. However, the binding of BCR/abl to p85 SH2 domains was abolished in cells expressing mutant, temperature-sensitive (ts) p210 BCR/abl in which the tyrosine in the YXXM motif of p210 BCR/abl was replaced by histidine. Despite lack of direct interaction with p85 **SH2 domains**, **expression** of ts p210 BCR/abl resulted in rapid, time-dependent activation of total and membrane-associated PI 3-kinase and increased PI 3-kinase activity in anti-P-tyr and anti-abl immunoprecipitates. These data suggest that BCR/abl-induced activation of PI 3-kinase in hematopoietic cells does not require binding of p85 SH2 domains to BCR/ abl gene product and involves interaction with other tyrosine phosphorylated intermediate proteins.

L11 ANSWER 12 OF 17 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 3
AN 1995:340392 BIOSIS
DN PREV199598354692
TI PTB domain binding to signaling proteins through a sequence motif containing phosphotyrosine.
AU Kavanaugh, W. Michael; Turck, Christoph W.; Williams, Lewis T. (1)
CS (1) Chiron Corp., 4560 Horton St., Emeryville, CA 94608 USA
SO Science (Washington D C), (1995) Vol. 268, No. 5214, pp. 1177-1179.
ISSN: 0036-8075.
DT Article
LA English
AB Src homology 2 (SH2) domains mediate assembly of signaling complexes by binding specifically to tyrosine-phosphorylated proteins. A phosphotyrosine binding (PTB) domain has been identified which also binds specifically to tyrosine-phosphorylated targets, but is structurally different from **SH2 domains**. **Expression** cloning was used to identify targets of PTB domains. PTB domains bound to phosphotyrosine within a sequence motif, asparagine-X-1-X-2-

phosphotyrosine (where X represents any amino acid), that is found in many signaling proteins and is not recognized by SH2 domains. Mutational studies indicated that high affinity binding of PTB domains may require a specific conformation of the motif.

L11 ANSWER 13 OF 17 CABA COPYRIGHT 2002 CABI
AN 94:82807 CABA
DN 940104662
TI Stat3 and Stat4: members of the family of signal transducers and activators of transcription
AU Zhong, Z.; Wen, Z.; Darnell, J. E., Jr.
CS Laboratory of Molecular Cell Biology, Rockefeller University, New York, NY 10021, USA.
SO Proceedings of the National Academy of Sciences of the United States of America, (1994) Vol. 91, No. 11, pp. 4806-4810. 29 ref.
ISSN: 0027-8424
DT Journal
LA English
AB The nucleotide and deduced amino acid sequences were determined for 2 members of the STAT (signal transducers and activators of transcription) family of proteins, STAT3 and STAT4, in mice. There were several highly conserved regions with 2 previously described genes (Stat91 and Stat113), including putative SH3 and **SH2 domains**.
Expression of the Stat4 gene in mice was restricted to testis, thymus and spleen. Stat4 was expressed in many tissues. Antiserum to STAT3 detected a major protein of approximately 92 kDa and a minor protein of approximately 89 kDa. Antiserum to STAT4 detected a major protein of approximately 89 kDa.

L11 ANSWER 14 OF 17 DGENE (C) 2002 THOMSON DERWENT
AN ABN84266 DNA DGENE
TI Novel purified and isolated Shc binding protein designated protein expressed in activated lymphocytes, useful as tumor markers for diagnosing cancer, and for treating hematopoietic stem cell disorders -
IN McGlade J; Schmandt R
PA (AMGE-N) AMGEN CANADA INC.
PI US 6399747 B1 20020604 50p
AI US 1999-363708 19990729
PRAI US 1998-83587 19980521
DT Patent
LA English
OS 2002-546297 [58]
AB The present sequence is a nested 3' RACE primer. The sequence is based on a cDNA clone isolated from an HeLa library screen using mouse PAL (protein expressed in activated lymphocytes) cDNA. 5' and 3' RACE were performed to obtain the full-length human PAL coding sequence given in ABN84261. PAL binds specifically to the Shc **SH2 domain**
. **Expression** is restricted to tissues containing actively dividing cells and to proliferating cells in culture. A role for the protein in signalling pathways governing cell cycle progression is suggested. PAL is more highly expressed in tumour cell lines than in normally proliferating cell lines, suggesting that PAL, or nucleic acids encoding it, may serve as tumour markers for diagnosing cancer and localizing tumour cells. PAL may also be used as a target in test systems to screen for drugs that block the promotion of cell proliferation, especially drugs for cancer treatment. PAL may also be used therapeutically to stimulate cell proliferation either by gene therapy or by the use of PAL polypeptides to stimulate haematopoiesis in vivo or ex vivo.

L11 ANSWER 15 OF 17 DGENE (C) 2002 THOMSON DERWENT
AN ABN84265 DNA DGENE
TI Novel purified and isolated Shc binding protein designated protein expressed in activated lymphocytes, useful as tumor markers for

diagnosing cancer, and for treating hematopoietic stem cell disorders -
IN McGlade J; Schmandt R
PA (AMGE-N) AMGEN CANADA INC.
PI US 6399747 B1 20020604 50p
AI US 1999-363708 19990729
PRAI US 1998-83587 19980521
DT Patent
LA English
OS 2002-546297 [58]
AB The present sequence is an outer 3' RACE primer. The sequence is based on a cDNA clone isolated from an HeLa library screen using mouse PAL (protein expressed in activated lymphocytes) cDNA. 5' and 3' RACE were performed to obtain the full-length human PAL coding sequence given in ABN84261. PAL binds specifically to the Shc **SH2 domain** . **Expression** is restricted to tissues containing actively dividing cells and to proliferating cells in culture. A role for the protein in signalling pathways governing cell cycle progression is suggested. PAL is more highly expressed in tumour cell lines than in normally proliferating cell lines, suggesting that PAL, or nucleic acids encoding it, may serve as tumour markers for diagnosing cancer and localizing tumour cells. PAL may also be used as a target in test systems to screen for drugs that block the promotion of cell proliferation, especially drugs for cancer treatment. PAL may also be used therapeutically to stimulate cell proliferation either by gene therapy or by the use of PAL polypeptides to stimulate haematopoiesis in vivo or ex vivo.

L11 ANSWER 16 OF 17 DGENE (C) 2002 THOMSON DERWENT
AN ABN84264 DNA DGENE
TI Novel purified and isolated Shc binding protein designated protein expressed in activated lymphocytes, useful as tumor markers for diagnosing cancer, and for treating hematopoietic stem cell disorders -
IN McGlade J; Schmandt R
PA (AMGE-N) AMGEN CANADA INC.
PI US 6399747 B1 20020604 50p
AI US 1999-363708 19990729
PRAI US 1998-83587 19980521
DT Patent
LA English
OS 2002-546297 [58]
AB The present sequence is a nested 5' RACE primer. The sequence is based on a cDNA clone isolated from an HeLa library screen using mouse PAL (protein expressed in activated lymphocytes) cDNA. 5' and 3' RACE were performed to obtain the full-length human PAL coding sequence given in ABN84261. PAL binds specifically to the Shc **SH2 domain** . **Expression** is restricted to tissues containing actively dividing cells and to proliferating cells in culture. A role for the protein in signalling pathways governing cell cycle progression is suggested. PAL is more highly expressed in tumour cell lines than in normally proliferating cell lines, suggesting that PAL, or nucleic acids encoding it, may serve as tumour markers for diagnosing cancer and localizing tumour cells. PAL may also be used as a target in test systems to screen for drugs that block the promotion of cell proliferation, especially drugs for cancer treatment. PAL may also be used therapeutically to stimulate cell proliferation either by gene therapy or by the use of PAL polypeptides to stimulate haematopoiesis in vivo or ex vivo.

L11 ANSWER 17 OF 17 DGENE (C) 2002 THOMSON DERWENT
AN ABN84263 DNA DGENE
TI Novel purified and isolated Shc binding protein designated protein expressed in activated lymphocytes, useful as tumor markers for diagnosing cancer, and for treating hematopoietic stem cell disorders -
IN McGlade J; Schmandt R

PA (AMGE-N) AMGEN CANADA INC.
PI US 6399747 B1 20020604 50p
AI US 1999-363708 19990729
PRAI US 1998-83587 19980521
DT Patent
LA English
OS 2002-546297 [58]
AB The present sequence is an outer 5' RACE primer. The sequence is based on a cDNA clone isolated from an HeLa library screen using mouse PAL (protein expressed in activated lymphocytes) cDNA. 5' and 3' RACE were performed to obtain the full-length human PAL coding sequence given in ABN84261. PAL binds specifically to the Shc **SH2 domain** . **Expression** is restricted to tissues containing actively dividing cells and to proliferating cells in culture. A role for the protein in signalling pathways governing cell cycle progression is suggested. PAL is more highly expressed in tumour cell lines than in normally proliferating cell lines, suggesting that PAL, or nucleic acids encoding it, may serve as tumour markers for diagnosing cancer and localizing tumour cells. PAL may also be used as a target in test systems to screen for drugs that block the promotion of cell proliferation, especially drugs for cancer treatment. PAL may also be used therapeutically to stimulate cell proliferation either by gene therapy or by the use of PAL polypeptides to stimulate haematopoiesis in vivo or ex vivo.

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